

GenCore version 5.1.6

卷之三

11

卷之三

111

卷之三

10

SUMMARIES

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	Length DB	ID	Description
1	1470	100.0	1470	6	AX114641 Sequence AX15641
2	505	34.4	2682	8	CAU64206 Candida albicans
3	153	10.4	2188	8	AF001978 Candida a
4	136.2	9.3	42565	8	CAC55AS
5	91.2	6.2	86265	3	AL034556 Plasmid
6	86.8	5.2	10492	2	AC005504 Plasmid
7	86.8	5.9	169546	2	AC004157 Plasmid
8	86.8	5.0	205421	3	AE014849 Plasmid
9	77.6	5.3	105682	3	AC116957_3
10	75.2	5.1	302156	3	AC116977 Dictyostelium
11	74.6	5.1	343050	3	PFM13P3
12	74	5.0	76558	3	MBREV
13	73.8	5.0	25063	3	AE014826
14	73.4	5.0	14867	3	AE01398
15	73.4	5.0	164397	3	PFM13P6
16	72.8	4.9	80803	3	AC135522 Homo sapi
17	72.8	5.0	113880	3	PFM13P4
18	72.6	4.9	110000	2	PFM13TP1_07
19	72	4.9	8055	2	AX590046
20	72	4.9	349751	3	PFM14P3
21	71.8	4.9	145992	9	AC114919
22	71.8	4.9	343050	3	PFM13P3
23	71.4	4.9	25568	3	AC116955
24	71.4	4.9	39984	3	AC116101
25	70.8	4.8	2009	6	AX457067
26	70.8	4.8	271546	3	AE014843
27	70.4	4.8	192929	3	AC005505
28	70.4	4.8	192713	3	AE014850
29	70.2	4.8	281723	3	PPA29359
30	69.4	4.7	182870	3	AC116960
31	69.2	4.7	253307	3	PFM13P7
32	68.6	4.7	166719	9	AC116957
33	68.6	4.7	18434	9	AC116994
34	68.2	4.6	192187	3	AC116920
35	68	4.6	9810	6	AX345328
36	67.8	4.5	250029	3	AE014830
37	67.6	4.6	170966	3	BR000991
38	67.4	4.6	66993	2	AC118074
39	67.2	4.6	1708	8	AF500786
40	67.2	4.5	7347	1	AF211124
41	67.2	4.6	67970	3	PFM13P3
42	67.2	4.6	110000	2	PFM13TP1_04
43	67	4.6	8055	6	AX590046
44	67	4.6	11000	2	AL052955_2
45	67	4.6	122838	2	BX248494
					Danio rerio

ALIGNMENTS

29:	em_vrl:*	RESULT	1
30:	em_htg_hum:*	AX15641	
31:	em_htg_inv:*	LOCUS	
32:	em_htg_other:*	DEFINITION	Sequence 1 from Patent WO0138550.
33:	em_htg_mus:*	ACCESSION	AK154641
34:	em_htg_pnt:*	VERSION	AK154641.1 GI:14536200
35:	em_htg_rnd:*	KEYWORDS	
36:	em_htg_mam:*	SOURCE	<i>Candida albicans</i>
37:	em_htg_vrt:*	ORGANISM	<i>Candida albicans</i>
38:	em_syr:*		<i>Ascomycota; Saccharomycotina; Saccharomycetes;</i>
39:	em_htgo_hum:*		<i>Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;</i>
40:	em_htgo_mus:*		<i>Saccharomycetales; mitosporic Saccharomycetales; Candida.</i>
41:	em_htgo_other:*	REFERENCE	1
		AUTHORS	Sundström, P.

CC diabetic ketoacidosis and patients in which the normal microflora has been disrupted because of disease, trauma or chemical, microbial, radiation or other immunosuppressive prophylaxis. Also provided is a method for characterising genes under control of a DNA binding protein

Db	901 TACTATAGCTCAACAAATTATCTTCATAAATGTTAAACAGTCATCTATAAT	960	PT antigen, epitope or therapeutic agent, or detecting genes or the presence of <i>Candida</i> in a sample.
Qy	961 TCTTGGATCCAAACAGGAACTGGAAATTGGATTCGAGATAATCGACTCACATC	1020	PT
Db	961 TCTTGGATCCAAACAGGAACTGGAAATTGGATTCGAGATAATCGACTCACATC	1020	XX
Qy	1021 ATGTAAGAGGAGACTTCTGAGCTCATATGCTTAATGCTTAATGACTCTAA	1080	PS
Db	1021 ATGTAAGAGGAGACTTCTGAGCTCATATGCTTAATGCTTAATGACTCTAA	1080	XX
Qy	1081 TCTAAACAAACAAACCTTCTAAACTATATACCTATGCTTAATGACTCTAA	1140	CC
Db	1081 TCTAAACAAACAAACCTTCTAAACTATATACCTATGCTTAATGACTCTAA	1140	CC
Qy	1141 GATAA-GTTAGTAGGCCAGCTGTTTTTGCCATTATTTGACTCATTTGTT	1199	CC
Db	1141 GATAA-GTTAGTAGGCCAGCTGTTTTTGCCATTATTTGACTCATTTGTT	1199	CC
Qy	1200 TCTTGTGAGCTTTATACCTTTGCACTCTCTTGATCCGTATTCACATTG	1259	CC
Db	1200 TCTTGTGAGCTTTATACCTTTGCACTCTCTTGATCCGTATTCACATTG	1259	CC
Qy	1260 GCTTTTTACATGAACTCTGTAAGGCTTTCCACTATTACATC	1319	CC
Db	1260 GCTTTTTACATGAACTCTGTAAGGCTTTCCACTATTACATC	1319	CC
Qy	1261 GCTTTTTACATGAACTCTGTAAGGCTTTCCACTATTACATC	1320	CC
Db	1320 TCTAAATGATCAGATGTTCAAACTATAATAGCTTAAATACCGC	1379	CC
Qy	1321 TGAATATGATCAAGATAGTTCAAACTATAATAGCTTAAATACCGC	1380	CC
Qy	1380 TATTTCATTCATCACTGTTCTCACATATCAACACAGAACTCT	1439	CC
Db	1381 TATTTCATTCATCACTGTTCTCACATATCAACACAGAACTCT	1440	CC
Qy	1440 ATAGTCAGCTGCCTTGTGCTCAGT	1470	CC
Db	1441 ATAGTCAGCTGCCTTGTGCTCAGT	1471	CC
RESULT 2			
AA57996/c			
ID	AA57996 standard; DNA; 2093 BP.		
XX			
AC	AA57996;		
XX			
DT	10-OCT-2000 (first entry)		
XX			
DB	2093 bp <i>Candida albicans</i> retrotransposon 15 sequence.		
XX			
KW	Retrotransposon; pCal; TC2; T ¹ ; copia; long terminal repeat; LTR; gag gene; group antigen; polyprotein; pol; aspartate protease; integrase; reverse transcriptase; RNaseH; Pseudoknot; readthrough translation; stop codon suppression; gene delivery; gene therapy vector; genetic vaccine composition; immunogenic; transgenic animal; ds.		
XX			
OS	<i>Candida albicans</i> .		
XX			
PN	WO200026397-A1.		
XX			
PD	11-MAY-2000.		
XX			
PF	01-NOV-1999; 99WO-NZ2000179.		
XX			
KW	gag gene; group antigen; polyprotein; pol; aspartate protease; integrase; reverse transcriptase; RNaseH; Pseudoknot; readthrough translation; stop codon suppression; gene delivery; gene therapy vector; genetic vaccine composition; immunogenic; transgenic animal; ds.		
XX			
RESULT 3			
AB210245/c			
ID	AB210246 standard; DNA; 8056 BP.		
XX			
AC	AB210246;		
XX			
DT	16-JAN-2003 (first entry)		
XX			
DE	Haematopoietic cell proliferation disorder related DNA sequence #386.		
XX			
KW	Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200277272-A2.		
XX			
Novel retrotransposon expression vectors useful for expressing an			

PD XX 03-OCT-2002.

PP XX 26-MAR-2002; 2002WO-EPO03401.

XX PR 26-MAR-2001; 2001US-0279333P.

PA XX (EPIG-) EPIGENOMICS AG.

PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J; Olek A, Piipenbrock C, Adorjan P, Grabs G, Lesche R, Leu S, Mueller V, Otto T, Pelet C; Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C; Schwoppe I, Ziebarth H;

XX DR WPI; 2003-018942/01.

PT Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.

XX PS Claim 28: SEQ ID NO 386; 117pp; English.

CC The present invention describes a method for detecting and differentiating between hematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. AB209861 to AB21118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative lympho-lymphatic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients.

XX SQ Sequence 8056 BP; 3711 A; 0 C; 3711 G; 3974 T; 0 U; 0 Other;

Query Match 4,9%; Score 72; DB 7; Length 8056; Best local Similarity 42.0%; Pred. No. 0.00051; Mismatches 670; indels 5; Gaps 1;

Matches 489; Conservative 0; Mismatches 670; indels 5; Gaps 1;

QY 203 TGGACCTTACGCGCATATAATTGGCGGATAACTGCCATAAAACTCTTGAC 262

Db 1640 TTACGATTCATTTCAATTTCATTTTAAATTTAAATTTAAATTTAAAT 1581

QY 263 ATACGATGTTCTTCACTGGAAATTGCT---TTTTACAGTA 317

Db 1580 ATTAAATTAAATTAATTTTAAATAATTTTAAATTTTAACTAT 1521

QY 318 TGAACATTGAAAGAAAGGAAAGGAAAGGAAAGGAAAGTGGCTAACATTGAAAT 377

Db 1520 TTATTTTATTTATTTATAATTAAATTAAATTAAATTAAATTAAATTAAATT 1461

QY 378 AGGCTTAAGGTTTCTGATGGCTTAACTAAAGGAAATAACAAAGTATTAGCGAT 437

Db 1460 AAAAATAATTTTATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT 1401

QY 438 AACCTGGTAGGAAAGTGTGACAAATAATTTGGCGGTAGCTTATGAAATAATGAA 497

Db 1400 ATATTTTATTTATAAAATAATAATAATAATAATAATAATAATAATAATAATA 1341

QY 498 ACTAAATCTTAAAGAATTCTCTTATATAAGGAATCCCTCTACAGGAGCTG 557

Db 1340 TTTTTAAATTTATAATAATAATAATAATAATAATAATAATAATAATAATA 1281

QY 558 ATATCCATCTGAAATTACGCGCACTAACTCCATCAATAATAGATGTTGATGTT 617

Db 1280 TTATATTTATTTATAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT 1221

QY 618 TCTCTGAGTAAATTCTACATTATGAACTGATCTGATTTTTCAGTTTCAAAATTTAT 677

Db 1160 ATTTATTTAAATTTCAAAATAATTAAATTTAAATTTAAACAAATAATTAACATTA 1101

QY 738 TCTAACAAAGTGTCCAGATTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT 797

Db 1100 AACATTAATAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1041

QY 798 GATGATGATTAACATGACTGACTGTTGAGTAAGATCAATTTTCAATTTTCAAT 857

Db 1040 AATTTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 981

QY 858 CGACTAATGCACTTACATCAGTCACTGGGTTGTTGCTCTACTATAAGCTCAACA 917

Db 980 ATTTTATTCATTTAAATAAAATAATAATAATAATAATAATAATAATAATAATAATA 921

QY 918 AATATCTTCATAAACTTAAATTAACAGTCATATACTCTTGGATCRAAAC 977

Db 920 CAACTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 861

QY 978 AACGAAATGGAATTCTGAGATAATGCGATAATGCGACTCACATCATTGAAAGGGAG 1037

Db 860 ATAAATAAAACAAATTTTTAAATAATAATAATAATAATAATAATAATAATAATA 801

CC 740 TTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 741

CC 800 AAATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 741

QY 1098 CTTCTAAACCTATAATTAACCTTAACTGGCTACACCGCTAATGTTAGTGGCC 1157

Db 1158 AGCTGTTTTTGCTTATTTTAACTATTTAAATTTAAATTTAAATTTAAATTTAAAT 681

QY 680 ATTTTTTTTTTTATAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT 621

Db 1218 TTATACCTTTGCAACTCTCTGTTACCTGGTTCCGGCTTTAACATAGCA 1277

Db 620 TTATATATAATTTATAATTTATAATTTATAATTTATAATTTATAATTTATAATTTATAAT 561

QY 1278 ACTCTGTAAGTCCTTCCTCCACATTATCATCTCTGAAATGTTACATGAG 133

Db 560 ATATAATTTATAATTTATAATTTATAATTTATAATTTATAATTTATAATTTATAAT 501

QY 1338 ATATTTTCAAAACTATTTATA 1361

Db 500 ATTTAATTTTTATTTATAATA 477

RESULT 4

ABU32425/c ID ABU32426 standard; DNA; 9810 BP.

XX AC XX

XX DT XX

XX Human immune system associated gene SEQ ID NO: 399.

XX Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antiarrhythmic; curostic; notropic; neuroprotective; anti-HRV; anticonvulstant; ophthalmological; antiarrhythmic; antiarrhythmic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;